



10079709 .110302

#6

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Robert F.M. Van Gorcom  
Willem Van Hartingsveldt  
Petrus A. Van Paridon  
Annemarie E. Veenstra  
Rudolf G.M. Luttin  
Gerardus Selten
- (ii) TITLE OF INVENTION: Cloning and Expression of Microbial  
Phytase
- (iii) NUMBER OF SEQUENCES: 52
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Morrison & Foerster
  - (B) STREET: 545 Middlefield Road, Suite 200
  - (C) CITY: Menlo Park
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94025-3471
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
(EPO)
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 07/688,578
  - (B) FILING DATE: 24-MAY-1991
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Murashige, Kate H.
  - (B) REGISTRATION NO: 29,959
  - (C) REFERENCE/DOCKET NUMBER: 24615-20026.00
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-327-7250
  - (B) FACSIMILE: 415-327-2951

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gln Ser Ser Xaa Asp Thr Val Asp Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Ser Xaa Xaa Gln Ser Ser Xaa Asp Thr Val Asp Gln Gly Tyr Gln  
1 5 10 15

Arg Phe Ser Glu Thr Ser His Leu Arg Xaa Gln Tyr Ala Pro Phe Phe  
20 25 30

Asp Leu Ala  
35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Val Asp Glu Arg Phe Pro Tyr Thr Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln	Xaa	Gln	Ala	Glu	Gln	Glu	Pro	Leu	Val	Arg	Val	Leu	Val	Asn	Asp
1				5				10						15	
Arg Val Val Pro															
20															

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa	Ser	Phe	Asp	Thr	Ile	Ser	Thr	Ser	Thr	Val	Asp	Thr	Lys	Leu	Ser
1				5				10						15	
Pro Phe Cys Asp Leu Phe Thr															
20															

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu	Ala	Val	Pro	Ala	Ser	Arg	Asn	Gln	Ser	Ser	Gly	Asp	Thr	Val	Asp
1				5				10						15	

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (v) FRAGMENT TYPE: internal

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Met	Gln	Cys	Gln	Ala	Glu	Gln	Glu	Pro	Leu	Val	Arg	Val	Leu	Val
1				5					10					15	
Asn Asp Arg															

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (v) FRAGMENT TYPE: internal

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala	Ser	Ser	Ala	Glu	Lys	Gly	Tyr	Asp	Leu	Val	Val
1				5					10		

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (v) FRAGMENT TYPE: internal

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Val Asp Xaa Arg Phe Pro Tyr Thr Gly Xaa Ala  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 Phytase N-terminus reverse  
 translation

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

YTNGCNGTNC CNGCNWSNMG NAAYCARWSN WSNGGNGAYA CNGTNGAYCA RGGNTAYCAR 60  
 MGNTTWWWSA RACNWSNCAW YTNMGNGGNC ARTAYGCNCC NTTYTTYGAY YTNGCN 116

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 internal fragment A (Phytase)  
 reverse translation

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CARNNNCARG CRGANCARGA RCCRYTNGTN HSNGTNYTNG TNRAYVVNVK NGTNCCNCCN 60  
 ATGGGN 66

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 99 base pairs  
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
internal fragment B (Phytase)  
reverse translation

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGGWSNTTYG AYACNATHWS NACNWSNACN GTNGAYACNA ARYTNWSNCC NTTYTCYGAY 60

YTNTTYACNA CNGAYGARTG YATHAMNTAY VGNTAYYTN 99

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
alkaline phosphatase reverse  
translation

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTYWSNTAYG GNGCNGCNAT HCCNCARWSN ACNCARGARA ARCARTTYWS NCARGARTTY 60

MGNGAYGGN 69

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AB1024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTGGTCGACG GTGTCGCCGC TGCTCTGGTT GCGGCTGGCG GGGACGGC

48

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AB1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGRTCCACG GTGTCGCC

18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AB1066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGRTCGACG GTGTCGCC

18

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AB1067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGRTCCACA GTGTCGCC

18

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AB1069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGRTCCACG GTATCGCC

18

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AB1069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTGGTCCACG GTGTCACC

18

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)



(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AB1070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTGATCGACA GTATCACC

18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AB1226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTGGTARCCC TGRTCSAC

18

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AB1227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

YTGRTADCCY TGRTCAC

18

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AB1298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

YTGRTASCCK TGRTCSACSG TRTC

24

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:  
AB1388
- (xi) SEQUENCE DESCRIPTION: SEQ ID N

ARGTCGAAGA ASGGSGCGTA CTGSCC

26

(2) INFORMATION FOR SEQ ID NO:25:

```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 23 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
      AB1295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
```

ACSARSGGYT CYTGYTCSGC YTG

23

(2) INFORMATION FOR SEQ ID NO:26:



(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - AB1026
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGGAAYTCCT GVSWGAAC TG CTTYTCCTG

29

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - AB1027
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGSGGRATN GCNCGRCCGT A

21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6756 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Aspergillus ficuum (Aspergillus niger)  
(B) STRAIN: NRRL 3135

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: lambda AF  
(B) CLONE: pAF2-3, pAF2-6, pAF2-7

(ix) FEATURE:

(A) NAME/KEY: exon  
(B) LOCATION: 210..253

(ix) FEATURE:

(A) NAME/KEY: intron  
(B) LOCATION: 254..355

(ix) FEATURE:

(A) NAME/KEY: exon  
(B) LOCATION: 356..1715

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: join(210..253, 356..1715)  
(D) OTHER INFORMATION: /codon\_start= 210  
/product= "Phytase"

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 210..380

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 381..1712  
(C) IDENTIFICATION METHOD: experimental  
(D) OTHER INFORMATION: /function= "inositol phosphate  
phosphatase"  
/product= "Phytase"  
/evidence= EXPERIMENTAL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCGACTTCC CGTCCTATTC GGCCTCGTCC GCTGAAGATC CATCCCACCA TTGCACGTGG	60
GCCACCTTTG TGAGCTTCTA ACCTGAACTG GTAGAGTATC ACACACCATG CCAAGGTGGG	120
ATGAAGGGGT TATATGAGAC CGTCCGGTCC GGC GCGATGG CCGTAGCTGC CACTCGCTGC	180
TGTGCAAGAA ATTACTTCTC ATAGGCATC ATG GGC GTC TCT GCT GTT CTA CTT	233
Met Gly Val Ser Ala Val Leu Leu	
-23 -20	
CCT TTG TAT CTC CTG TCT GG GTATGCTAAG CACCACAATC AAAGTCTAAT	283
Pro Leu Tyr Leu Leu Ser Gly	
-15 -10	
AAGGACCCTC CCTTCCGAGG GCCCCTGAAG CTCGGACTGT GTGGGACTAC TGATCGCTGA	343

CTATCTGTGC AG A GTC ACC TCC GGA CTG GCA GTC CCC GCC TCG AGA AAT	392
Val Thr Ser Gly Leu Ala Val Pro Ala Ser Arg Asn	
-8 -5 1	
CAA TCC AGT TGC GAT ACG GTC GAT CAG GGG TAT CAA TGC TTC TCC GAG	440
Gln Ser Ser Cys Asp Thr Val Asp Gln Gly Tyr Gln Cys Phe Ser Glu	
5 10 15 20	
ACT TCG CAT CTT TGG GGT CAA TAC GCA CCG TTC TTC TCT CTG GCA AAC	488
Thr Ser His Leu Trp Gly Gln Tyr Ala Pro Phe Phe Ser Leu Ala Asn	
25 30 35	
GAA TCG GTC ATC TCC CCT GAG GTG CCC GCC GGA TGC AGA GTC ACT TTC	536
Glu Ser Val Ile Ser Pro Glu Val Pro Ala Gly Cys Arg Val Thr Phe	
40 45 50	
GCT CAG GTC CTC TCC CGT CAT GGA GCG CGG TAT CCG ACC GAC TCC AAG	584
Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Asp Ser Lys	
55 60 65	
GGC AAG AAA TAC TCC GCT CTC ATT GAG GAG ATC CAG CAG AAC GCG ACC	632
Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Ala Thr	
70 75 80	
ACC TTT GAC GGA AAA TAT GCC TTC CTG AAG ACA TAC AAC TAC AGC TTG	680
Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser Leu	
85 90 95 100	
GGT GCA GAT GAC CTG ACT CCC TTC GGA GAA CAG GAG CTA GTC AAC TCC	728
Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn Ser	
105 110 115	
GGC ATC AAG TTC TAC CAG CGG TAC GAA TCG CTC ACA AGG AAC ATC GTT	776
Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile Val	
120 125 130	
CCA TTC ATC CGA TCC TCT GGC TCC AGC CGC GTG ATC GCC TCC GGC AAG	824
Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly Lys	
135 140 145	
AAA TTC ATC GAG GGC TTC CAG AGC ACC AAG CTG AAG GAT CCT CGT GCC	872
Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg Ala	
150 155 160	
CAG CCC GGC CAA TCG TCG CCC AAG ATC GAC GTG GTC ATT TCC GAG GCC	920
Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu Ala	
165 170 175 180	
AGC TCA TCC AAC AAC ACT CTC GAC CCA GGC ACC TGC ACT GTC TTC GAA	968
Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe Glu	
185 190 195	
GAC AGC GAA TTG GCC GAT ACC GTC GAA GCC AAT TTC ACC GCC ACG TTC	1016
Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr Phe	
200 205 210	
GTC CCC TCC ATT CGT CAA CGT CTG GAG AAC GAC CTG TCC GGT GTG ACT	1064

Val	Pro	Ser	Ile	Arg	Gln	Arg	Leu	Glu	Asn	Asp	Leu	Ser	Gly	Val	Thr		
		215					220					225					
CTC	ACA	GAC	ACA	GAA	GTG	ACC	TAC	CTC	ATG	GAC	ATG	TGC	TCC	TTC	GAC	1112	
Leu	Thr	Asp	Thr	Glu	Val	Thr	Tyr	Leu	Met	Asp	Met	Cys	Ser	Phe	Asp		
		230				235					240						
ACC	ATC	TCC	ACC	AGC	ACC	GTC	GAC	ACC	AAG	CTG	TCC	CCC	TTC	TGT	GAC	1160	
Thr	Ile	Ser	Thr	Ser	Thr	Val	Asp	Thr	Lys	Leu	Ser	Pro	Phe	Cys	Asp		
		245			250					255					260		
CTG	TTC	ACC	CAT	GAC	GAA	TGG	ATC	AAC	TAC	GAC	TAC	CTC	CAG	TCC	TTG	1208	
Leu	Phe	Thr	His	Asp	Glu	Trp	Ile	Asn	Tyr	Asp	Tyr	Leu	Gln	Ser	Leu		
				265					270					275			
AAA	AAG	TAT	TAC	GGC	CAT	GGT	GCA	GGT	AAC	CCG	CTC	GGC	CCG	ACC	CAG	1256	
Lys	Lys	Tyr	Tyr	Gly	His	Gly	Ala	Gly	Asn	Pro	Leu	Gly	Pro	Thr	Gln		
			280					285					290				
GGC	GTC	GGC	TAC	GCT	AAC	GAG	CTC	ATC	GCC	CGT	CTG	ACC	CAC	TCG	CCT	1304	
Gly	Val	Gly	Tyr	Ala	Asn	Glu	Leu	Ile	Ala	Arg	Leu	Thr	His	Ser	Pro		
		295					300					305					
GTC	CAC	GAT	GAC	ACC	AGT	TCC	AAC	CAC	ACT	TTG	GAC	TCG	AGC	CCG	GCT	1352	
Val	His	Asp	Asp	Thr	Ser	Ser	Asn	His	Thr	Leu	Asp	Ser	Ser	Pro	Ala		
		310				315					320						
ACC	TTT	CCG	CTC	AAC	TCT	ACT	CTC	TAC	GCG	GAC	TTT	TCG	CAT	GAC	AAC	1400	
Thr	Phe	Pro	Leu	Asn	Ser	Thr	Leu	Tyr	Ala	Asp	Phe	Ser	His	Asp	Asn		
		325			330					335					340		
GGC	ATC	ATC	TCC	ATT	CTC	TTT	GCT	TTA	GGT	CTG	TAC	AAC	GGC	ACT	AAG	1448	
Gly	Ile	Ile	Ser	Ile	Leu	Phe	Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr	Lys		
				345				350						355			
CCG	CTA	TCT	ACC	ACG	ACC	GTG	GAG	AAT	ATC	ACC	CAG	ACA	GAT	GGA	TTC	1496	
Pro	Leu	Ser	Thr	Thr	Thr	Val	Glu	Asn	Ile	Thr	Gln	Thr	Asp	Gly	Phe		
			360					365					370				
TCG	TCT	GCT	TGG	ACG	GTT	CCG	TTT	GCT	TCG	CGT	TTG	TAC	GTC	GAG	ATG	1544	
Ser	Ser	Ala	Trp	Thr	Val	Pro	Phe	Ala	Ser	Arg	Leu	Tyr	Val	Glu	Met		
		375				380						385					
ATG	CAG	TGT	CAG	GCG	GAG	CAG	GAG	CCG	CTG	GTC	CGT	GTC	TTG	GTT	AAT	1592	
Met	Gln	Cys	Gln	Ala	Glu	Gln	Glu	Pro	Leu	Val	Arg	Val	Leu	Val	Asn		
		390				395					400						
GAT	CGC	GTT	GTC	CCG	CTG	CAT	GGG	TGT	CCG	GTT	GAT	GCT	TTG	GGG	AGA	1640	
Asp	Arg	Val	Val	Pro	Leu	His	Gly	Cys	Pro	Val	Asp	Ala	Leu	Gly	Arg		
					405		410			415				420			
TGT	ACC	CGG	GAT	AGC	TTT	GTG	AGG	GGG	TTG	AGC	TTT	GCT	AGA	TCT	GGG	1688	
Cys	Thr	Arg	Asp	Ser	Phe	Val	Arg	Gly	Leu	Ser	Phe	Ala	Arg	Ser	Gly		
				425				430						435			
GGT	GAT	TGG	GCG	GAG	TGT	TTT	GCT	TAGCTGAATT	ACCTTGATGA	ATGGTATGTA						1742	
Gly	Asp	Trp	Ala	Glu	Cys	Phe	Ala										

440

445

TCACATTGCA	TATCATTAGC	ACTTCAGGTA	TGTATTATCG	AAGATGTATA	TCGAAAGGAT	1802
CAATGGTGAC	TGTCACTGGT	TATCTGAATA	TCCCTCTATA	CCTCGTCCCA	CAACCAATCA	1862
TCACCCTTTA	AACAATCACA	CTCAACGCAC	AGCGTACAAA	CGAACAAACG	CACAAAGAAT	1922
ATTTTACTACT	CCTCCCCAAC	GCAATACCAA	CCGCAATTCA	TCATACCTCA	TATAAATACA	1982
ATACAATACA	ATACATCCAT	CCCTACCCTC	AAGTCCACCC	ATCCTATAAT	CAATCCCTAC	2042
TTACTTACTT	CTCCCCCTCC	CCCTCACCCCT	TCCCAGAACT	CACCCCCGAA	GTAGTAATAG	2102
TAGTAGTAGA	AGAAGCAGAC	GACCTCTCCA	CCAATCTCTT	CGGCCTCTTA	TCCCCATACG	2162
CTACACAAAA	CCCCCACCCC	GTTAGCATGC	ACTCAGAAAA	TAATCAAAAA	TAAC TAAGAA	2222
GGAAAAAANA	GAAGAAGAAA	GGTTACATAC	TCCTCTCATA	CAAAC TCCAA	GACGTATACA	2282
TCAAGATGGG	CAATCCCACC	ATTACTGATA	TCCATCTATG	AACCCATTCC	CATCCCACGT	2342
TAGTTGATTA	CTTTACTTAG	AAGAAGAAAA	AGGGAAGGGA	AGGGAAAGAA	GTGGATGGGA	2402
TTGAGTTAGT	GCTCACCGTC	TCGCAGCAAG	TTTATATTCT	TTTGT TTTGGC	GGATATCTTT	2462
CACTGCTCCT	GCTGGACGTT	GTCACGGGGT	GGTAGTGGTT	GGCGGTGGTG	AGGGTCCATG	2522
ATCACTCTTG	GTTTGGGGGG	TTGTTGTTGT	CGTTGTTGTT	GTTGTTGGGT	GGGCATTTTC	2582
TTTCTTCAC	TTGGGGATTA	TTATTTGGAA	TTGGTTAGTT	TGAGTGAGTG	GGTAATATTG	2642
AATGGGTGAT	TATTGGGAAT	GAAGTAGATT	TGGCTATGAA	TGGTTGATGG	GATGGAATGA	2702
ATGGATGGAT	GAATAGATGG	AGGCGGAAAA	GTCAGGTGGT	TTGAGGTTCG	GATTATTATC	2762
TTTGTGCCTG	AGGCATCACT	CTCCATCTAT	GTTGTTCTTT	CTATACCGAT	CTACCAGAGC	2822
TAAGTTGACT	GATTCTACCA	CAGTGCACAA	TAAGTATGTA	CTTATTTTCAT	TTAGAGTATT	2882
TAGATTAACC	CGCTGTGCTA	TTTGCCGTAG	CTTTCCACCC	AATTTGGAAG	TTCGAAGAAT	2942
TAAAACTCAT	CCTACAGTAC	AGAATAGAAG	TAAAAGGAGA	AGAGAAAAAC	AAGATAATAC	3002
AACCAGTCCA	GGTCCATTCT	AGATCTCGAA	TGACCACCAA	ATAAGAAAAGC	AACAAGCAAG	3062
TAAGCAAAGC	ATAAGTCTAA	ATGAACGCCA	ATAACTTCAT	CGCCTGCCTT	TGAAACTGAA	3122
CGCTATGCAC	GAATGGCTCG	AAATGATTCC	CTTAACTCCG	TAGTATTGAG	AGTGAGAGGA	3182
AAAGAAAAAA	AGAGACAGAA	AAGCTGACCA	TGGGAAAGAA	GCATGATCAG	TCGGGAATGG	3242
ATCTGCGGGT	TGAGATAGAT	ATGAGTTGCC	TCGCAGATCC	GGTGACAAGA	TAAGAGAATT	3302
GGGAGATGTG	ATCAGCCACT	GTAAC TTCAT	CAAGCATCGA	CATTCAACGG	TCGGGTCTGC	3362
GGGTTGAGAT	GCAAGTTGAG	ATGCCACGCA	GACCCGAACA	GAGTGAGAGA	TGTGAGACTT	3422



TTGAACCACT	GTGACTTCAT	CAAGCATCAA	AACACACTCC	ATGGTCAATC	GGTTAGGGTG	3482
TGAGGGTTGA	TATGCCAGGT	TCGATGCCAC	GCAGACCCGA	ACCGACTGAG	AAATATGAAA	3542
AGTTGGACAG	CCACTTCATC	TTCATCAAGC	GTAAAACCCC	AATCAATGGT	AAATCGAAAA	3602
CGAATCTGCG	GGCTGATGTG	GAAATGAGAC	GAATGCCTCG	CAGATTTCGAA	GACACGTAAA	3662
TCGAGATGAA	CAATCACTTT	AACTTCATCA	AAGCCTTAAA	TCACCCAATG	GCCAGTCTAT	3722
TCGGGTCTGC	GGGTTGAGGT	TCCTGTTGAG	ATGCCACGCA	GACTGCGAAC	ATGCGATGCA	3782
TTATAAGTTG	GACGAGTGTA	GACTGACCAT	TGATAACCGA	GATAAACAAT	CACTTCAACT	3842
TCATCAAAGC	CTTAAATCAC	TCAATGGCCA	GTCTGTTTGC	GGTCTGCGGG	CTGATACCCA	3902
AGTTGCGATG	CCACGCAGAC	TGCAAAACATT	GATCGAGAGA	CGAGAAAAAC	AACGCACTTT	3962
AACTTCAACA	AAAGCCTTTC	AATCAGTCAA	TGGCCAGTCT	GTTGCGGGTC	TGCGGGCTGA	4022
TATGCGAGTT	GAGGTGCCTC	GCAGACCGCG	AACATGCGAT	GTAATTTCTT	AGTTAGACGA	4082
GTGCCTGGCC	ATTGAGAAAC	GAGAGAAACA	ACCACTTTAA	CTTCATGAAA	GCCTTGAACT	4142
ACTCAATGAC	CCGTCTGTTG	GCGGTCTGCG	GGCTGATATT	CGAGTTGAGA	TGCCACGCAG	4202
ACCGCCAACA	TGCGATGTAT	CATGTAAGTT	AGATGAGTGA	CTGGCCATTG	AGAAACGAGA	4262
GAAACAACCA	CACTTCATGA	GAGCCTTAAA	TTATTCAATG	ACCAGTCTGT	TCACGGTCTG	4322
CGGGTTGGTA	TGCGAGTCGA	GGTGCCTCGC	AGACCGCGAA	CATGCGATGT	TTTCGATGGA	4382
CGAGTGAAGC	CTGACGATCG	AGAACTATCT	CAGTTGGGTT	GGCCATTCGG	CTGGCCGTTG	4442
GGTTTAGTAT	TAGGATCGTC	AGGTTTGTCC	GATGGAACGT	TCCGTTTGCG	TGCGTTGGCG	4502
CGACGAGCCC	TCTCCTCGGC	GTGATTCTGA	AATTCTGCAA	TCAGGGCAGC	CGCAGCACGG	4562
CGACGGGACG	TCCTCCAGGA	GCTGTGTTGA	AGTTTCGGGG	TGGCGGTCCA	GAAGGGGGAG	4622
TTACATTAAA	AGCCTCATAG	ATGTCTTTGG	GTGGTTCCGG	GGGGCCCATC	GCAAGATCTT	4682
CTGGAGTTGT	GCGTCTGATC	ATCTCTTGAG	TGTAATTGCG	ACGCAGACCG	AGCTTCAGGA	4742
TTTTGGAAGG	GCTGGATCGC	TCCTGCTGAC	TCTTTCCTC	AGCGGGCTTC	GTCTCGGCAG	4802
TCTTCATTTT	GGCGGGCTGA	TCTTCCATCT	CAGAATGGGA	TCGCTTCTG	GTCGCTGCAC	4862
CCGCTCCTCC	CTTCAAGGTC	AGCTTGATGC	GCAGCGTCTT	GGGCGGCTCA	GCTGGTGGAG	4922
TTGGTTCCGG	CTCTGGCTCC	CTCCGGCGTC	GCTTGGGCAC	TTGAGTAGTC	TCTGAGGCTT	4982
CGCCGCGGCG	CCGTTTGCGA	GTCCGCTCCT	TGGTCTCTTT	GGCCTCTTTC	ACTTCACCTG	5042
GACCGTCTTT	CGGGGCGGTT	TCATCGTGCT	GAGCGATCAA	GGTTTGATG	TAGGCAGCCG	5102

GCATCATTCG ATCAACGGCA ATTCCTCTCT TCGGGGCCTC CTCCCAGGCC TTGATTGTCG 5162

CCTTGACCTC GTCCACGTTT TCGAAGAAGA AAGGCATCTT GTTATCCTGA GGCAAGTTGC 5222

GCTCTCCCAT GCGTGGGGAT ATCCGAAGAT GCGGTCTTC TCGAACTGTT CATGAGACTT 5282

CAGACGAATT GGAGGCTGGG GGAGCAATTT GTCTCCGTAG GTGTTGTTAG GGCGGAACCA 5342

AGAATAGCCT TCGCCTACAA CGACAAGCTC TTCGCCAAAT TTATTTTTTTT GGCCTGTAAA 5402

AACGAACCCA TCCTCGTCAG TCCACCGGTG CGTCTCGGAC GTAGAGATTG GCTTACTTAT 5462

TCCCTCAACG CCGATCTCTG CCTGGGGCTG CGCTTCGGAT GCGGCCTCGG TCACGGCTCC 5522

GCCTCGGACT GCACCGCTGG AGTTTCGGTC TTCTTCTCCT GCTTCTCCAG GTACTCCTTG 5582

CGTAACTCTT CGATCAGCCT CGGCTTCCGA TGA CTGCTCA AATTCTGGAG CAACAGCTGC 5642

CGCGGCCAGG TCAAGCAGGC GGTTTGCTAA AACTGCCCCAT TTTCCATCGA CACCTGCCTC 5702

CGACGCCTGT GCAA AACCAG CTGTTTTCGC ATTGGCCTGT TTGTTGGCAC GCGTCTTCTT 5762

GA CTGCTGCC TTGCCCTTTA CTCCTTGAG AGCAGACTCT GGCTTAGATG ATGGTGACG 5822

GTTTCTGCGG AAGCGCCGCT CAGATTCCAA AGATTCCATA GCTTTAATGG TAGGCTTTCT 5882

GGTCTTCCA GAAGTGCGCG CAGCTGACGT AGTGGTTGAG TAGCTGGCAG TTGGGGATCC 5942

TGGGCCCTCA TTGGAACCAT CAAGACCAA TTTGTTTCCA TACATATCAG CATGGTATTC 6002

AAAAGGAAAA CTTTCGCCGT ACGGAGTACT GCGTTCGATT CCGGGTGAT CCAAGTCGTA 6062

TCCAGACATG GTGTGCAATT CAGCCTTGCT GTCAAGAGCA GGGGTACTTT CAATGCTGTC 6122

AGCAACCACG CGGCCAAAGG GCGTCTTCGG GAAAGAAGGT GTTCAAGAG AAGCGTCATC 6182

CACGGCCTGG CTTGCGGCGT TGATTGCAGA CTTTCGAGTA GATCGCTGAG GTCGCGAACT 6242

GGTTCGAGTA GCAACCTGTG AATTGGCAGC CTTGTGACTG CTTGATTCA CTGCAGAGAC 6302

GGAGTAGACT GCACTGATTT GGAATTCTGA GTCGCAGCCA TTCTGGATTT GCGTTCGGCG 6362

CGACGAGATC TCGCAGTCGT GGTACGAGGA GTAGAGCGAG GCTGCGTAGC AGTGTGCAA 6422

GCTTGGTGCT AGCCTCCTGG GCTTCAGCAG CTTCAGCAGT GGTGGCAGAC GCAGCAGAAT 6482

TAGCGGAGCT TTATCGGCTT TGCCGCTCTG AGCGTTGGGA GTAGAAGTGA GAGAAGAGGT 6542

AGAGTCCACG GAAGAAGTCT TCTCGCTGTT CTCAAAGCCG TTCAGCTTTG CTGGCATAGA 6602

CTTACGCGTC TTGCGGCTGT TGGAAGCGGA AGAGTTCATG GCGGGAGAGG AGACGTTAGA 6662

AGTAGACATG GTGGGGTTTG TTGACGGGTT TTGAGTAACA AGAGACTTGC GTCGATCTTT 6722

GAGTGTCTT GACAGAAAGT TATGCAACGT CGAC 6756

[illegible]

(A) LENGTH: 467 amino acids

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Arg Leu Glu Asn Asp Leu Ser Gly Val Thr Leu Thr Asp Thr Glu

220                      225                      230  
 Val Thr Tyr Leu Met Asp Met Cys Ser Phe Asp Thr Ile Ser Thr Ser  
 235                      240                      245  
 Thr Val Asp Thr Lys Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp  
 250                      255                      260                      265  
 Glu Trp Ile Asn Tyr Asp Tyr Leu Gln Ser Leu Lys Lys Tyr Tyr Gly  
 270                      275                      280  
 His Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly Tyr Ala  
 285                      290                      295  
 Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val His Asp Asp Thr  
 300                      305                      310  
 Ser Ser Asn His Thr Leu Asp Ser Ser Pro Ala Thr Phe Pro Leu Asn  
 315                      320                      325  
 Ser Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile Ile Ser Ile  
 330                      335                      340                      345  
 Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr  
 350                      355                      360  
 Thr Val Glu Asn Ile Thr Gln Thr Asp Gly Phe Ser Ser Ala Trp Thr  
 365                      370                      375  
 Val Pro Phe Ala Ser Arg Leu Tyr Val Glu Met Met Gln Cys Gln Ala  
 380                      385                      390  
 Glu Gln Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro  
 395                      400                      405  
 Leu His Gly Cys Pro Val Asp Ala Leu Gly Arg Cys Thr Arg Asp Ser  
 410                      415                      420                      425  
 Phe Val Arg Gly Leu Ser Phe Ala Arg Ser Gly Gly Asp Trp Ala Glu  
 430                      435                      440  
 Cys Phe Ala

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus ficuum* (*Aspergillus niger*)

(B) STRAIN: NRRL 3135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGGGCGTCT CTGCTGTTCT ACTTCCTTTG TATCTCCTGT CTGGAGTCAC CTCCGGACTG	60
GCAGTCCCCG CCTCGAGAAA TCAATCCAGT TGCGATACGG TCGATCAGGG GTATCAATGC	120
TTCTCCGAGA CTTCGCATCT TTGGGGTCAA TACGCACCGT TCTTCTCTCT GGCAAACGAA	180
TGGGTCATCT CCCCTGAGGT GCGCGCCGGA TGCAGAGTCA CTTTCGCTCA GGTCTCTCTC	240
CGTCATGGAG CGCGGTATCC GACCGACTCC AAGGGCAAGA AATACTCCGC TCTCATTGAG	300
GAGATCCAGC AGAACGCGAC CACCTTTGAC GGAAAATATG CCTTCCTGAA GACATACAAC	360
TACAGCTTGG GTGCAGATGA CTTGACTCCC TTCGGAGAAC AGGAGCTAGT CAACTCCGGC	420
ATCAAGTTCT ACCAGCGGTA CGAATCGCTC ACAAGGAACA TCGTTCCATT CATCCGATCC	480
TCTGGCTCCA GCCGCGTGAT CGCCTCCGGC AAGAAATTCA TCGAGGGCTT CCAGAGCACC	540
AAGCTGAAGG ATCCTCGTGC CCAGCCCGGC CAATCGTCGC CCAAGATCGA CGTGGTCATT	600
TCCGAGGCCA GCTCATCCAA CAACACTCTC GACCCAGGCA CCTGCACTGT CTTCGAAGAC	660
AGCGAATTGG CCGATACCGT CGAAGCCAAT TTCACCGCCA CGTTCGTCCC CTCCATTCTG	720
CAACGTCTGG AGAACGACCT GTCCGGTGTG ACTCTCACAG ACACAGAAGT GACCTACCTC	780
ATGGACATGT GTCCTTTCGA CACCATCTCC ACCAGCACCG TCGACACCAA GCTGTCCCCC	840
TTCTGTGACC TGTTACCCA TGACGAATGG ATCAACTACG ACTACCTCCA GTCCTTGAAA	900
AAGTATTACG GCCATGGTGC AGGTAACCCG CTCGGCCCGA CCCAGGGCGT CGGCTACGCT	960
AACGAGCTCA TCGCCCGTCT GACCCACTCG CCTGTCCACG ATGACACCAG TTCCAACCAC	1020
ACTTTGGACT CGAGCCCGGC TACCTTTCCG CTCAACTCTA CTCTCTACGC GGACTTTTCG	1080
CATGACAACG GCATCATCTC CATTCTCTTT GCTTTAGGTC TGTACAACGG CACTAAGCCG	1140
CTATCTACCA CGACCGTGGA GAATATCACC CAGACAGATG GATTCTCGTC TGCTTGACG	1200
GTTCCGTTTG CTTCGCGTTT GTACGTCGAG ATGATGCAGT GTCAGGCGGA GCAGGAGCCG	1260
CTGGTCCGTG TCTTGTTTAA TGATCGCGTT GTCCCGCTGC ATGGGTGTCC GGTGATGCT	1320
TTGGGGAGAT GTACCCGGA TAGCTTTGTG AGGGGGTTGA GCTTTGCTAG ATCTGGGGGT	1380
GATTGGGCGG AGTGTTTTGC TTAG	1404

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTAGAATT CAAAAATGGG CGTCTCTGCT GTTCTA

36

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGTGACGAAT TCGTGCTGGT GGAGATGGTG TCG

33

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGCACCAAG CTGAAGGATC C

21

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAACTGCAGG CGTTGAGTGT GATTGTTTAA AGGG

34

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AG-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GACAATGGCT ACACCAGCAC CGCAACGGAC ATTGTTTGGC CC

42

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
AG-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAGCAGCCAT TGCCCGAAGC CGAT

24

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTCTGCAGGA ATTCAAGCTA G

21

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
18-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGAGGCGGGG ACTGCCAGTG CCAACCCTGT GCAGAC

36

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
18-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCTGCACAG GGTTGGCACT GGCAGTCCCC GCCTCG

36

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGCACGAGGA TCCTTCAGCT T

21

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AATTCAAGCT TG

12

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

24-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGAGCCGGGG ACTGCCAGGC GCTTGAAAT CACATT

36

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
24-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AATGTGATTT CCAAGCGCCT GGCAGTCCCC GCCTCG

36

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
fyt-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AACAGCAGAG ACGCCCATTTG CTGAGGTGTA ATGATG

36

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
fyt-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CATCATTACA CCTCAGCAAT GGGCGTCTCT GCTGTT

36

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCTTCCCCG GTAC

14

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGCTCCCCCG GATC

14

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGCTAGGGGG

10

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TCGACCCCCT